



Pig Genome Update Special

No. 114 November 15, 2012

This little piggy went to publication!!

The Swine Genome Sequencing Consortium is pleased to announce the publication of a high quality draft genome sequence for the pig (*Sus scrofa*). The paper entitled “*Analyses of pig genomes provide insight into porcine demography and evolution*” describing the sequencing, analysis and annotation of this draft genome sequence is published in Nature. In parallel a series of companion papers has been published in BMC journals.

The genome paper reports analyses not only of the reference genome of Duroc 2-14 aka TJ Tabasco but also analyses of genomes of several wild boars and other domesticated pigs. The analyses revealed a deep phylogenetic split between European and Asian wild boars dating back ~1 million years. This observation, in part, provides final justification for the wide trait mapping crosses developed in the 1990s, especially between Western and Chinese breeds. It was argued at the time that Chinese and Western pigs were as genetically divergent as *Mus musculus* and *Mus spretus* species of mice which had been extensively used in mouse genetics research. In effect, this judgment has been validated.

As observed in other genomes, genes encoding immune response functions show evidence of rapid evolution. The pig has the largest repertoire of functional olfactory receptor genes of any mammal sequenced to date – perhaps that is why they are effective hunters for truffles. There is evidence that genes involved in taste are located in pig evolutionary break points. Pigs can tolerate higher levels of substances that are distasteful to humans – perhaps the ability of pigs to eat material that is unpalatable to humans was one of the attractions when they were domesticated.

A comparison of multiple pig genomes and the comparison of pig and human genomes reveal several potentially disease-causing genetic variants which may extend the value of pigs in biomedical research.

The pig industry has an excellent track record for rapid and effective exploitation of new knowledge and technologies. The pig genome sequence is expected to enable the acceleration of pig genetics research, the results of which are expected to be translated into pig improvement in a timely manner. The pig industry support for the sequencing project is gratefully acknowledged by the Consortium.

This paper represents an important landmark for the Consortium which was launched back in 2003. For many of the authors their collaborative research in pig genetics and genomics stretches back to the early 1990s and the European PiGMaP project and USDA Pig Genome Coordinated activities in the US. The project has benefited from these long established collaborations and friendships. Transnational funding was critical to the delivery of the project, including USDA funding to The Wellcome Trust Sanger Institute, European Commission and European Research Council funding and significant contributions from Korean, Japanese and Chinese national sources and many others

including several US universities and industry partners which are all acknowledged in the paper. The draft pig genome sequence, the pig genome paper and associated companion papers are important achievements for the pig research community, but there is more still to learn and do (kindly provided by Alan Archibald, Martien Groenen, and Larry Schook On behalf of the Swine Genome Sequencing Consortium).

Congratulations go to not only the authors, donors and contributors for this effort to produce the paper but also the many colleagues over the past years who have contributed to the pig genome research efforts worldwide.

*Max F. Rothschild
U.S. Pig Genome Coordinator
2255 Kildee Hall
Department of Animal Science
Iowa State University
Ames, Iowa 50011
Phone/Fax: 515-294-6202
mfrothsc@iastate.edu*

Supported by Multi-State Research Funds to the National Research Service Program: NRSP-8. National Animal Genome Research Program, Lakshmi Matukumalli , NAGRP Director, NIFA